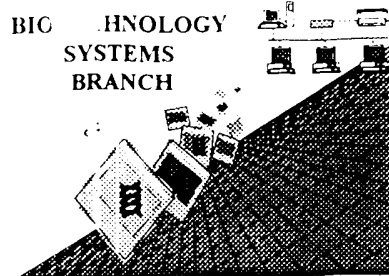


BEST AVAILABLE COPY

RAW SEQUENCE LISTING
ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/806,708
Source: P4/09
Date Processed by STIC: 4/16/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/806,703

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 _____ Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
<400> sequence id number
000
- 10 _____ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 _____ Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES) Valid response is Artificial Sequence
- 12 _____ Use of <220>Feature Sequence(s) _____ are missing the <220>Feature and associated headings
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 _____ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing)
Instead, please use "File Manager" or any other means to copy file to floppy disk

PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/806,708

DATE: 04/16/2001
TIME: 09:26:05

Input Set A:\58741 seq.txt
Output Set N:\CRF3\04122001\I806708.raw

Does Not Comply
Correct in Filing Office Needed

3 <110> APPLICANT: The University of British Columbia
5 <120> TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
7 <130> FILE REFERENCE: 4810-58741
9 <140> CURRENT APPLICATION NUMBER: US/09/806,708
10 <141> CURRENT FILING DATE: 2001-04-03
12 <150> PRIOR APPLICATION NUMBER: US 60/147,133
13 <151> PRIOR FILING DATE: 1999-08-04
15 <160> NUMBER OF SEQ ID NOS: 23
17 <170> SOFTWARE: PatentIn version 3.0

ERRORED SEQUENCES

643 <210> SEQ ID NO: 23
644 <211> LENGTH: 1055
645 <212> TYPE: DNA
646 <213> ORGANISM: Artificial sequence
648 <220> FEATURE:
649 <221> NAME/KEY: promoter
650 <222> LOCATION: (1)..(1055)
651 <223> OTHER INFORMATION: consensus sequence of A.t. and L.a. FAEI promoters
654 <400> SEQUENCE: 23

W--> 655	actsakwaaa	rmyakyagwt	(nntgtrttkgt	tgktwyycan	gtgkrcyarr	wgkmttayym	60
W--> 657	tatkwtgttgw	awrtwrwaam	kktrkwcst	amnnawttmc	tarkwrtgtr	wwtktnnnat	120
W--> 659	gtrwrtgywm	tnnnngcstnt	warryktrrw	wcytamwyga	swagnastrr	ttytwwrkwm	180
W--> 661	ckrksarara	trgrarymra	wytawarrtg	wtkamayaaw	tmnnnnnnak	aackrattwg	240
W--> 663	wraksnctct	taggtttkra	tccwaytoga	gwatkkwktw	ktsaamgwtw	nnnnnnnttt	300
W--> 665	tkaamyaaar	wmwwsatttw	waaawtsrkt	wtyygrktam	nnnnngttcwt	rmwawtwkmw	360
W--> 667	mktkgtttwn	nnggrtytgw	ttkkmathtt	akanncttaa	wkwtctmnn	ttaakattyw	420
W--> 669	atcywksmtn	gtsyryaaar	ytwyawwtrr	yayannnnnk	ttwkactwtt	ykrccttann	480
W--> 671	taawytkssa	nctsrtrtrwk	tncwragstk	asmgrayara	ywtgykwnta	waywctwyy	540
W--> 673	yragawwtam	ymmtsateyc	ataattagtc	agaggstakg	nnnnnnnnnc	caatcarwkc	600
W--> 675	taasaacama	nattcyctya	annatytwan	natgcwnatk	taatmwtnnn	nnnagtwtnn	660
W--> 677	nnnnakmasa	atwyaaaamt	aatkyaartan	ttamagayar	aaayttrtan	ngactttttt	720
W--> 679	nnttggmrtn	taaargwann	nnnnnnnnnn	ngacwawrtt	tatanegtnn	nnnnnnnnay	780
W--> 681	atttntatatt	twwrtrkann	nnnnnnaaay	ygaaawknnt	tmcwctkawm	kawatgaatt	840
W--> 683	tnagtatatn	nnnnnatatt	tytkyaatng	kactayttts	ctattttggc	amctttcaky	900
W--> 685	kgactactam	tttattwcaa	tgtgtatgsa	tgcatgagyy	tgagtantac	acatgtctaw	960
W--> 687	atrmatgcwt	ngyaaaacgt	aacggaccac	aaaagwggat	ccatrcaaata	acatctcatm	1020
W--> 689	gcwycctenn	nnnnntccg	acacaaancw	garca			1055
E--> 692							
E--> 695							

see
item 10
on Encl
summary
sheet

(first two
lines are
samples of
env. throughout
sequence 2.3)

delete at end of file

FJI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/806,708

DATE: 04/16/2001

TIME: 09:26:07

Input Set : A:\58741 seq.txt

Output Set: N:\CRF3\04122001\I806708.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:55 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID# 3
L:79 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID# 4
L:85 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID# 5
L:100 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID# 6
L:115 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID# 7
L:139 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID# 8
L:145 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID# 9
L:169 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID# 10
L:175 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID# 11
L:199 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID# 12
L:205 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID# 13
L:229 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID# 14
L:592 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:594 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:596 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:598 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:610 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:614 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:616 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:618 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:622 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:628 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:636 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 22
L:655 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 23
L:657 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 23
L:659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 23
L:661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 23
L:663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 23
L:665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 23
L:667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 23
L:669 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 23
L:671 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 23
L:673 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 23
L:675 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 23
L:677 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 23
L:679 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 23
L:681 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 23

VERIFICATION SUMMARY

DATE: 04/16/2001

PATENT APPLICATION: US/09/806,708

TIME: 09:26:07

Input Set : A:\58741 seq.txt

Output Set: N:\CRF3\04122001\I806708.raw

L:683 M 341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:685 M 341 W: (46) "n" or "Xaa" used, for SEQ ID# 23
L 687 M 341 W: (46) "n" or "Xaa" used, for SEQ ID# 23
L 689 M 341 W: (46) "n" or "Xaa" used, for SEQ ID# 23
L 692 M 254 E: No. of Bases conflict, LENGTH:Input:1 Counted:1055 SEQ:23
M:254 Repeated in SeqNo=23